



1 / 3

```
AMSH1 THNEFTITHVIVP--KQSAGPDYCDMENVEELFNVQDQHD--LLTLGWIIHPTQTAFLS
AMSH2 THNEFTITHVIVP--KQSAGPDYCDMENVEELFNVQDQHD--LLTLGWIIHPTQTAFLS
AMSH MRNEFTITHVLIP--KQSAGSDYCNTEEEELFLIQDQOG--LITLGWIIHPTQTAFLS
Rpn11 TVRVIDVFAMPQS--GTGVSVEAVDPVFQAKMLDMLKQTGRPEMVVGWYHSHPGFGCWLS
Jab1 TMIIMDSFALPVEGTETRVNAQAAAYEYMAAYIENAKQVGRLENAIGWYHSHPGYGCWLS
      :      :      .. :      :      . * .      . : * * * : * * *      . : * *

AMSH1 SVDLHTHCSYQLMLPEAIAIVCSPKHKDTG-----IFRLTNAGMLEVSACKKKGFH--PH
AMSH2 SVDLHTHCSYQLMLPEAIAIVCSPKHKDTG-----IFRLTNAGMLEVSACKKKGFH--PH
AMSH SVDLHTHCSYQMLPESVAIVCSPKFQETG-----FFKLDHGLEEISSCRQKGFH--PH
Rpn11 GVDINTQQSFEALSERAVAVVDPIQSVKGKVVIDAFRLINANMMVLGHEPRQTTSNLGH
Jab1 GIDVSTQMLNQFQEPFVAVVIDPRTTISAG-----KVNLGAFRTYPKGYKPPDEGPSEYQ
      . : * : * : : : * : * . * . . . . . :

AMSH1 TKEPRLFSICKHV--LVKDIKI-----IVLDLR-----
AMSH2 TKEPRLFSIQKFLSGIISGTAL-----EMEPLKIGYGPNGFLLGISRSSSPSEQ
AMSH SKDPPLFCSCSHVT--VVDRAV-----TITDLR-----
Rpn11 LNKPSIQALIHGLNRHYYSITINYRKNELEQKMLLNHLHKKSWMEGLTLQDYSEHCKHNES
Jab1 TIPLNKIEDFGVHCKQYYALEVSYFKSSLDRKLELLWLNKYWVNTLSSSSLLTNADYTTG
      :      :      *

AMSH1 -----
AMSH2 L-----
AMSH -----
Rpn11 VVKEMLELAKNYNKAVEEEDKMTPEQLAIKNVGKQDPKRHLEEHVDVLMTSNIVQCLAAM
Jab1 QVFDLSEKLEQSEAQLGRGSFMLG--LETHDRKSEDKLAKATRDCKTTIEAIHGLMSQV

AMSH1 -----
AMSH2 -----
AMSH -----
Rpn11 LDTVVFVK-----
Jab1 IKDKLFNQINIS
```

FIG. 1



3 / 3

| | |
|---------------|---|
| COP9_su5_Hs | VGRLENAIGWYHSHPGYGCWLSGIDVSTQMLNQFQEPFVA--VVIDPTRTISAGKVNLG |
| COP9_su5_Dm | VGRMEHAVGWYHSHPGYGCWLSGINVSTQMLNQTYQEPFVA--IVVDPVRTVSAGKVCLG |
| COP9_su5_At | AGRLENVVGWYHSHPGYGCWLSGIDVSTQRLNQHQEPFLA--VVIDPTRTVSAGKVEIG |
| cop9_su5_Ce | EGRKEKVVGWYHSHPGYGCWLSGIDVSTQTLNQKFQEPWVA--IVIDPLRTMSAGKVDIG |
| AF2198_Arcfu | LPIGMKVFGTVHSHPSPPSCRPEEDLSLFTRFGKYHIIVCY--PYDENSWKCYNRKGEEV |
| PH0451_Pyrho | MPHDESIKGTFFHSHPSPPFPYSEGDLMFFSKFGGIHIIAAF--PYDEDSVKAFDSEGREV |
| TVN1035_Thevo | KPIDFSLVGSVHSHPSGITKPSDEDLRMFSLTGKIHIIVGY--PYNLKDYSAYDRSGNKV |
| MTH971_Metth | LPPFTGAVGSVHSHPGPVNLPAAADLHFFSKNGLFHLIIAH--PYTMETVAAYTRNGDPV |
| aq_1691_Aquae | ISKGMEIVGVYHSHPDHPDRPSQFDLQRAFPDLSYIIFSVQ--KGKVASYRSWELKGDKF |
| RV1334_Myctu | EDADEVPVVIYHSHTATEAYPSRTDVKLATEPDAHVVLVSTRDPHRHELRSYRIVDGAVT |
| RadC_Ecoli | IKINASALILAHNHPSGCAEPSKADKLITERIIKSCQFMDL--RVLDHIVIGRGEYVSFA |
| |'HSHP'.....'S 'D |

FIG. 3

| | |
|-------------|--|
| COP9_su5_Hs | VGRLENAIGWYHSHPGYGCWLSGIDVSTQMLNQFQEPFVA--VVIDPTRTISAGKVNLG |
| COP9_su5_Dm | VGRMEHAVGWYHSHPGYGCWLSGINVSTQMLNQTYQEPFVA--IVVDPVRTVSAGKVCLG |
| COP9_su5_At | AGRLENVVGWYHSHPGYGCWLSGIDVSTQRLNQHQEPFLA--VVIDPTRTVSAGKVEIG |
| cop9_su5_Ce | EGRKEKVVGWYHSHPGYGCWLSGIDVSTQTLNQKFQEPWVA--IVIDPLRTMSAGKVDIG |
| Pad1_Dm | TGRPEMVVGWYHSHPGFGCWLSGVDINTQQSFEALSERAVA--VVVDPIQSVKG-KVVID |
| Pad1_Hs | TGRPEMVVGWYHSHPGFGCWLSGVDINTQQSFEALSERAVA--VVVDPIQSVKG-KVVID |
| Sks1_Dd | TGRDEIVIGWYHSHPGFGCWLSVDVNTQQSFEQLQSRVA--VVVDPLQSVRG-KVVID |
| Pad1_Sc | TGRDQMVVGWYHSHPGFGCWLSVDVNTQKSFEQLNSRAVA--VVVDPIQSVKG-KVVID |
| |'HSHP'.....'S 'D |

FIG. 4